



180-158-2 seq listing rev2.ST25.txt
SEQUENCE LISTING

<110> Duke University
York, John D

<120> NOVEL TARGETS FOR LITHIUM THERAPY AND TOXICITY TREATMENT

<130> 180/158/2

<150> US 60/401480
<151> 2002-08-06

<160> 24

<170> PatentIn version 3.3

<210> 1
<211> 2113
<212> DNA
<213> Homo sapiens

<220>
<221> mRNA
<222> (1)..(2113)

<400> 1
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cgctttgct ctccttgaag tgtcttggt ccaacgttgt tccagagtgt accatggctt 120

ccagtaaacac tgtgttgatg cggttggtag cctccgcata ttctattgct caaaaggcag 180

gaatgatagt cagacgtgtt attgctgaag gagacctggg tattgtggag aagacctgtg 240

caacagacct gcagaccaaa gctgaccgat tggcacagat gagcatatgt tcttcattgg 300

cccgaaatt ccccaaactc acaattatacg gggaaagagga tctgccttct gaggaagtgg 360

atcaagagct gattgaagac agtcagtggg aagaaatact gaagcaacca tgcccatcgc 420

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agtacagtgc tattaaagaa gaagatctcg tggctctgggt tgatcctctg gatggaacca
480

aggaatatac cgaaggcttt cttgacaatg taacagtctt tattggatt gcttatgaag
540

gaaaagccat agcaggagtt attaaccagc catattacaa ctatgaggca ggaccagatg
600

ctgtgttggg gaggacaatc tggggagtt tagtttagg cgcccttggg tttcagctga
660

aagaagtccc tgctggaaa cacattatca caactactcg atcccatagc aacaagttgg
720

ttactgactg tgttgctgct atgaaccccg atgctgtgct gcgagtagga ggagcaggaa
780

ataagattat tcagctgatt gaaggcaaag cctctgctta tgtatttgca agtcctggg
840

gtaagaagtg ggataacttgt gctccagaag ttatttaca tgctgtgggaa ggcaagttaa
900

ccgatatcca tggaatgtt cttcagtaacc acaaggatgt gaagcatatg aactctgcag
960

gagtcctggc cacactgagg aattatgact actatgcaag ccgagttcca gaatcttatta
1020

aaaatgcact tgcccttaa aggaaagttt catttggccg ggccgcggcgg ctcatgcctg
1080

taatcccagc actttggag gccgaggcag gtggatcaact tgagctcagg agttgagac
1140

cagcctggc aatatcgtga gacccatct ctacaaaaat acaaattaac tggcatcct
1200

gtcatgcgcc tgtcatccca gctacttgag aggctgaagc agaagaatct cttgagcccg
1260

gaaggcggag gttgcagtga gctgagatcg tgccactgca ctccagcctg agtgcacagga
1320

gttaagccct gtctcagaaa aaaaacataa accaaaaaag tacttaaagt ttcatttact
1380

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tactaggaaa agacttggtt ctc当地ataat acatttaag attaatttggg tagaatttga
1440

gttccaccc ttcatgttt gacagtgatt tatatttagt tataatttta gaataaaaat
1500

taactaaata atttaacttg attaatacca ttactcaacc tgacaattga gttggagact
1560

tataaactca ttatggttat catgtgtttt cctgttgaat gtgaagaagt gagaaaaacat
1620

ttgccaatga cagttaggcg tgc当地actga ccattcactg ataaaccaga ttctgcctga
1680

atctgaaggg attgcttgta gcatagggtt tagtggcgtg atcttgggtc actgcggccc
1740

gcttccgggg ttc当地gttc tcctgcctag ctccgggtag ctgggactgc agcacggccc
1800

acgctggtaa tttttgtat gatggtgaga agtttcacc gtgttgccag gatggcttat
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cctgacatcg tgatctgtat gc当地cgatc ccaaagtgc当地 tggatgaca gctgtgagcc
1920

accgcacttg gcttaaacca gatttcttta gggcacattt ttttggatc tcactctgtt
1980

ttcacagta attttaaaaa cgtttatcc aattagaata tatatgatgt tattatata
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aaaaaaaaaaa aaa
2113

<210> 2
<211> 308
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE

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<222> (1)..(308)

<400> 2

Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
1 5 10 15

Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
20 25 30

Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr
35 40 45

Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg
50 55 60

Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu
65 70 75 80

Glu Val Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu
85 90 95

Lys Gln Pro Cys Pro Ser Gln Tyr Ser Ala Ile Lys Glu Glu Asp Leu
100 105 110

Val Val Trp Val Asp Pro Leu Asp Gly Thr Lys Glu Tyr Thr Glu Gly
115 120 125

Leu Leu Asp Asn Val Thr Val Leu Ile Gly Ile Ala Tyr Glu Gly Lys
130 135 140

Ala Ile Ala Gly Val Ile Asn Gln Pro Tyr Tyr Asn Tyr Glu Ala Gly
145 150 155 160

Pro Asp Ala Val Leu Gly Arg Thr Ile Trp Gly Val Leu Gly Leu Gly
165 170 175

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Ala Phe Gly Phe Gln Leu Lys Glu Val Pro Ala Gly Lys His Ile Ile
180 185 190

Thr Thr Thr Arg Ser His Ser Asn Lys Leu Val Thr Asp Cys Val Ala
195 200 205

Ala Met Asn Pro Asp Ala Val Leu Arg Val Gly Gly Ala Gly Asn Lys
210 215 220

Ile Ile Gln Leu Ile Glu Gly Lys Ala Ser Ala Tyr Val Phe Ala Ser
225 230 235 240

Pro Gly Cys Lys Lys Trp Asp Thr Cys Ala Pro Glu Val Ile Leu His
245 250 255

Ala Val Gly Gly Lys Leu Thr Asp Ile His Gly Asn Val Leu Gln Tyr
260 265 270

His Lys Asp Val Lys His Met Asn Ser Ala Gly Val Leu Ala Thr Leu
275 280 285

Arg Asn Tyr Asp Tyr Tyr Ala Ser Arg Val Pro Glu Ser Ile Lys Asn
290 295 300

Ala Leu Val Pro
305

<210> 3
<211> 364
<212> PRT
<213> Artificial

<220>
<223> Li-sensitive sequence uniting motif.

<220>
<221> MISC_FEATURE
<222> (2)..(41)

<223> X is any amino acid, and wherein between 0 and 39 of the residues
can be missing.

<220>

<221> MISC_FEATURE
<222> (44)..(143)

<223> X is any amino acid, and wherein between 0 and 99 of the residues
can be missing.

<220>

<221> MISC_FEATURE
<222> (146)..(146)

<223> X is isoleucine or an amino acid that can be conservatively substituted in place thereof.

<220>

<221> MISC_FEATURE
<222> (148)..(148)

<223> X is glycine or an amino acid that can be conservatively substituted in place thereof.

<220>

<221> MISC_FEATURE
<222> (149)..(149)

<223> X is threonine or an amino acid that can be conservatively substituted in place thereof.

<220>

<221> MISC_FEATURE
<222> (150)..(349)

<223> X is any amino acid, and wherein between 0 and 199 of the residues can be missing.

<220>

<221> MISC_FEATURE
<222> (350)..(350)

<223> X is tryptophan or an amino acid that can be conservatively substituted in place thereof.

<220>

<221> MISC_FEATURE
<222> (351)..(351)

<223> X is aspartic acid or an amino acid that can be conservatively substituted in place thereof.

<220>

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<221> MISC_FEATURE
<222> (352)..(362)
<223> X is any amino acid.

<400> 3

Asp Xaa
1 5 10 15

Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Glu Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa
50 55 60

Xaa
65 70 75 80

Xaa
85 90 95

Xaa
100 105 110

Xaa
115 120 125

Xaa Asp
130 135 140

Pro Xaa Asp Xaa
145 150 155 160

Xaa
165 170 175

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Xaa
180 185 190

Xaa
195 200 205

Xaa
210 215 220

Xaa
225 230 235 240

Xaa
245 250 255

Xaa
260 265 270

Xaa
275 280 285

Xaa
290 295 300

Xaa
305 310 315 320

Xaa
325 330 335

Xaa
340 345 350

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly
355 360

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<210> 4
<211> 290
<212> PRT
<213> Artificial

<220>
<223> Li-sensitive sequence uniting motif for Impasel.

<220>
<221> MISC_FEATURE
<222> (1)..(46)
<223> X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (48)..(69)
<223> X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (72)..(89)
<223> X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (96)..(218)
<223> X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (221)..(231)
<223> X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (234)..(290)
<223> X is any amino acid.

<400> 4

Xaa
1 5 10 15

Xaa Xaa

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20

25

30

Xaa Asp Xaa
35 40 45

Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Glu Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Pro Ile Asp Gly Thr Xaa
85 90 95

Xaa
100 105 110

Xaa
115 120 125

Xaa
130 135 140

Xaa
145 150 155 160

Xaa
165 170 175

Xaa
180 185 190

Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Asp Xaa Xaa Xaa Xaa

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210

215

220

Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225 230 235 240

Xaa
245 250 255

Xaa
260 265 270

Xaa
275 280 285

Xaa Xaa
290

<210> 5
<211> 399
<212> PRT
<213> Artificial

<220>
<223> Li-sensitive sequence uniting motif for lptase.

<220>
<221> MISC_FEATURE
<222> (1)..(53)
<223> X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (55)..(78)
<223> X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (81)..(152)
<223> X is any amino acid.

<220>

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<221> MISC_FEATURE
<222> (159)..(314)
<223> X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (317)..(327)
<223> X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (330)..(399)
<223> X is any amino acid.

<400> 5

Xaa
1 5 10 15

Xaa
20 25 30

Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Asp Xaa
50 55 60

Xaa Glu Glu
65 70 75 80

Xaa
85 90 95

Xaa
100 105 110

Xaa
115 120 125

180-158-2 seq listing rev2.ST25.txt

Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Pro Ile Asp Ser Thr Xaa Xaa
145 150 155 160

Xaa
165 170 175

Xaa
180 185 190

Xaa
195 200 205

Xaa
210 215 220

Xaa
225 230 235 240

Xaa
245 250 255

Xaa
260 265 270

Xaa
275 280 285

Xaa
290 295 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Asp Xaa Xaa Xaa Xaa
305 310 315 320

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
325 330 335

Xaa
340 345 350

Xaa
355 360 365

Xaa
370 375 380

Xaa
385 390 395

<210> 6
<211> 338
<212> PRT
<213> Artificial

<220>
<223> Li-sensitive sequence uniting motif for Fbpase1.

<220>
<221> MISC_FEATURE
<222> (1)..(74)
<223> X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (76)..(97)
<223> X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (100)..(118)
<223> X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (125)..(279)
<223> X is any amino acid.

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<220>
<221> MISC_FEATURE
<222> (282)..(292)
<223> X is any amino acid.
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<220>
<221> MISC_FEATURE
<222> (295)..(338)
<223> X is any amino acid.
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<400> 6

Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa .Glu Glu Xaa Xaa

Xaa Xaa Xaa Xaa Xaa Asp Pro Leu Asp Gly Ser Xaa Xaa Xaa Xaa
 115 120 125

180-158-2 seq listing rev2.ST25.txt

Xaa
145 150 155 160

Xaa
165 170 175

Xaa
180 185 190

Xaa
195 200 205

Xaa
210 215 220

Xaa
225 230 235 240

Xaa
245 250 255

Xaa
260 265 270

Xaa Xaa Xaa Xaa Xaa Xaa Tyr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
275 280 285

Xaa Xaa Xaa Xaa Gly Gly Xaa
290 295 300

Xaa
305 310 315 320

Xaa
325 330 335

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Xaa Xaa

<210> 7
<211> 53
<212> DNA
<213> artificial

<220>
<223> 5' DNA PCR primer.

<400> 7
ggatccgagc tcgaattcca ccatggagat ccccgggagc ctgtgcaaga aag
53

<210> 8
<211> 55
<212> DNA
<213> artificial

<220>
<223> 5' DNA PCR primer.

<400> 8
ggatccgtcg acgagctcgc ggccgcggtg gagtgactgg gttaacagcc taagc
55

<210> 9
<211> 49
<212> DNA
<213> artificial

<220>
<223> 5' DNA PCR primer

<400> 9
agatcttca attgaagctt gtcgaccagc atgtcgggga tcaagaagc
49

<210> 10
<211> 48
<212> DNA
<213> artificial

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<220>

<223> 5' DNA PCR primer.

<400> 10

agatctaaggc ttccgcggtc gacctggagc caaaggctta gttcttct
48

<210> 11

<211> 31

<212> DNA

<213> artificial

<220>

<223> 5' DNA PCR primer

<400> 11

ggatccatgc ctgctcctca cggtggatt c
31

<210> 12

<211> 43

<212> DNA

<213> artificial

<220>

<223> 5' DNA PCR primer.

<400> 12

ccgcgggtcga cgcggccgcg gtcgatcatg aattttgcc tac
43

<210> 13

<211> 31

<212> DNA

<213> artificial

<220>

<223> 5' DNA PCR primer.

<400> 13

ggatccaaggc acactgtaca ccaatggcta c
31

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<210> 14
<211> 42
<212> DNA
<213> artificial

<220>
<223> 5' DNA PCR primer.

<400> 14
gcggccgccc g cggtcgaccg gatcagaatt tcacggtaat cc
42

<210> 15
<211> 31
<212> DNA
<213> artificial

<220>
<223> 5' DNA PCR primer.

<400> 15
atcgatcata tggagccctt gcgtaaacca c
31

<210> 16
<211> 22
<212> DNA
<213> artificial

<220>
<223> 5' DNA PCR primer

<400> 16
tcatatttga cagcggAACG tg
22

<210> 17
<211> 981
<212> DNA
<213> artificial

<220>
<223> Fragment of BPntase genomic DNA located between exons 5 and 6
with 5' and 3' engineered restriction sites.

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<400> 17
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60

tacacttcct ttcctgaggg actgtgctga catgtctgac tgggctagag aaatgctcca
120

ccaccctgg tccccatagca tccccctcacc tgaggttgtc acaggtaaga aaaccagaag
180

gcatcgaatt aaatccagag gtgtaaaagt caggaggagt tgtgtgagag ctcacacctg
240

taatctcagc acactggggc agagggactg ctttgagttt gaggccatct tgagtgcata
300

acatggcaag ttctgggtca gcttgggtta gagcaagacc ttttcttaggc aaagcaagac
360

attagtcaga agaaccaggc ctcagagctg gacttcgggt tttatTTTtt tgTTTgtttg
420

tttttatttt ttgagacagg gtttctctgt gtagccctgg ttgtcctggc actcaCTTg
480

tagaccagac tggcctcgaa ctcagaaatc tgcctgcctc tgcctcccgaa gtgctggat
540

taaagggtgtg cgccaccact gcctggctta gacttcaagt ttAAAAGCC tagagttgt
600

gttttGAAAT aaagatctgc attgagaact tgtgaggctg aggcaggaag actgtgaggt
660

cagcctggcc ttcacagtga gtttcaggTC agcctgagat agaggagcag tgtgaggcca
720

gaaggacCCC acaaagaaag acctccacag cgctgcttct aacgggtcca gttcgagag
780

gctttctcac agctgccaga gagaatgttgc ttggcccctg gaggagatag agtataCTG
840

actctgtgtg tgtgtgtgt aatatataact gtatataactg tgagggtgca tgtgtgcaac
900

atgcataatgt actgtaaaaa tgtgtgagag gcagtgtgtt cgtatgtgtg tctgtgagta
960

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taaccatgc gtatgtatc t
981

<210> 18
<211> 35
<212> DNA
<213> artificial

<220>
<223> 5' DNA PCR primer

<400> 18
ggcgccgt agcacccac atactctccc agctc
35

<210> 19
<211> 34
<212> DNA
<213> artificial

<220>
<223> 3' DNA PCR primer

<400> 19
ggcgccag attacatacg catgggttat actc
34

<210> 20
<211> 4858
<212> DNA
<213> artificial

<220>
<223> Fragment of the genomic BPntase sequence with engineered 5' and
3' flanking restriction sites.

<400> 20
tggcgagctt gcttattctg ctttcagagt atgggttgtt ataaaggcactg tggcgccaca
60

ctgggttcc ccgactctta gcccattaa agcaggttgg aatcttagagc gttatgaaag
120

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agtttctcaa tttagagaaga gaatattcca aataattaa aagcacctt gcaaacttga
180

actgttgtgg agctggaaat gcagttcagt gtagtgccct gcttgtgtg tgtcaggggc
240

gtgtgtgatc tctatcagca cacacacaca cacacacacg cacgcacgca cgcacacaca
300

cacgcacgca cacacacacg cacacacgca cgcacacacg cgcgcacaca cacacacaca
360

cacacacaca cacacacgct gttttaaact atgattgtt attggatac agtttcacac
420

ggtagtacaa gctgatctca gattcatggc tgtccttcta tgtcctgata ttagagccgt
480

gcagtgctat ccagcctcac ttctcagtct ttttgtttt ttgtttgtt ttgtttgtt
540

ttgttttatt ttttgagac agggtttctc tgtgaagccc tggctgtcct ggaactcact
600

ctgttagacca ggctggcctc gaactcagaa atccgcctgc ctctgcctcc cgagtgctgg
660

gattaaaggc gtgcggcgcc acgccccggcg tcacttctca gtcttagctg ctgttacttc
720

tctgagaagc agcgagggcc ctcactagtt gatccctggg ctcgggtctg cgttatactg
780

gggagtcgga agactggta ccccgatttg tactgatacg gagatttgca ttcttggtta
840

cagacctcgg ccaccgacct gcagaccaaa gccgaccgct tggtgcagat gagcatatgc
900

tcttcctgg cccggaagtt cccgaagctg accatcatag gggaaagaggt gagaggcgcg
960

cgccacttgg attcataaccc tacctgccat tgagccgtag gttatggtca gtcttagcgt
1020

tggcactaac gttccaaacac aaagcgatcg tttccttag gggaaaaatc tgacttaatg
1080

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atattttggc ccacttaatg ggctaagtct ccatattctag tgatgggagc tatggtcacc
1140

attgtataac catacgatgg actcagtggc agaaagtcgc ctactgtatg tgaggctcta
1200

aggtgggaga catctcagtc ataagaccat gtggctaca tatgtgaggt cctgggttgg
1260

agcccctgca tcagcagtta tatgtgaaga gtcggcaagg ttctggaact ctgagatgac
1320

tgggcttggc ttgcttgc tgcattccgt catttcagat tggacttgc tacttacaac
1380

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1440

tgcatacatg taatacattc tgattccct catacttcgg attctcctcc cctcccccttc
1500

ttccttgcgc gccccctttt cccacttagt ttattcagga tcatccatgt gaccattca
1560

ttgggaccat ccattggca tcagtggc acagctgaaa gcaatggc ttcccttccc
1620

tgaatcagtc tgttaggaaat agttctgcag tgaaggagag agagtgcgg tctgcacatc
1680

tcctccacct ctgcttaact gttgggactc attcttctc agacccagca cagtcacatcg
1740

gttgttgaga gttcatgctt gcactggcgc gcacccagg aatgacgttt ggcagccctt
1800

ctccccgttt ttcagctttt accatcttc tgcccccttc ctacaaagcc tggtaaacct
1860

tagaggggat aaatgtctaa atatcttatt cagagctgag caatcagctg taagttgtc
1920

tttattaggcc ttcatatatc tctcccttca ttatagtcct ctagaaagag aatcttctct
1980

gactaaggct gagtggtaat tcgctatgtg aataaacatc tatattttagg aagctgtttg
2040

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acactgtgtg actttagtaa agctgttagag ttaactccc taagaggact catggcctcc
2100

cttttatac actgagtgaa tctccagaca tggagtgtgt ttaacgtact aagcgtggat
2160

tcccatgctg gagtagccct cacattcgat caagagcagg tagttacccc ccaacagtgc
2220

cgacactgtt gttgtaccag tgagcacagc ttgcctgaca gatggtgctg tagttgtca
2280

ggtcacaga tggcaatac tttctccccc agcagcctgc agagaaaatg tgttcaggc
2340

tgacttctt gtctcatgca accaaagtgt gtgggtcat tagcagtaag gtcttagcat
2400

ctaattgttag tggcaacca agaaaaatga caatgcctat attgtcttag ggcagtggga
2460

cctccgtgac caacttatca ggaggcacca cacacacagc aggtggggtt ttaatgaagg
2520

ataatttcac aggggagcag tttcttaggtc tctctttcc aactaaaaaa aatgcaccc
2580

agttattgtg agtaaattga aaatcaacag ataagttgtt ttccaacagt gcgtgtcag
2640

gcctctggac gtgtgaaaga cagcagtatt ccatgtactg ggatagctgg ccatgtgccg
2700

gaacagctgg gctacggatg ctgttcttag tggtaagg aattgccac ccagttcca
2760

tatggctgca ctggttccc accagcaatg aaggagtccc tctttccac cctcaccagg
2820

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2880

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180-158-2 seq listing rev2.ST25.txt

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180-158-2 seq listing rev2.ST25.txt

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180-158-2 seq listing rev2.ST25.txt

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<211> 24

<212> DNA

<213> artificial

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<212> DNA

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<223> DNA oligonucleotide for PCR screen

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24

180-158-2 seq listing rev2.ST25.txt